

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/060,294B
Source: 1FW16
Date Processed by STIC: 1/3/05

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/060,294B

DATE: 01/03/2005

TIME: 16:38:44

Input Set : A:\US09060294.txt

Output Set: N:\CRF4\01032005\I060294B.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Martin Roland Jensen
 7 Soren Mouritsen
 8 Henrik Elsner
 9 Iben Dalum

11 (ii) TITLE OF INVENTION: Modified human TNF-alpha molecules, DNA
 12 encoding them, and vaccines containing said modified
 13 TNF-alpha or DNA

15 (iii) NUMBER OF SEQUENCES: 44

17 (iv) CORRESPONDENCE ADDRESS:
 18 (A) ADDRESSEE: JACOBSON HOLMAN, PLLC
 19 (B) STREET: 400 Seventh St., N.W.
 20 (C) CITY: Washington
 21 (D) STATE: DC
 22 (E) COUNTRY: USA
 23 (F) ZIP: 20004

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk
 27 (B) COMPUTER: IBM PC compatible
 28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

31 (vi) CURRENT APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/09/060,294B

33 (B) FILING DATE: 15-Apr-1998

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 60/044,187

37 (B) FILING DATE: 24-APR-1997

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: William E. Player
 41 (B) REGISTRATION NUMBER: 31,409
 42 (C) REFERENCE/DOCKET NUMBER: P60953US1

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (202) 638-6666

46 (B) TELEFAX: (202) 393-5350

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 474 base pairs
 52 (B) TYPE: nucleic acid
 53 (C) STRANDEDNESS: double
 54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

58 (iii) HYPOTHETICAL: NO

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60 (iv) ANTI-SENSE: NO
62 (vi) ORIGINAL SOURCE:
63 (A) ORGANISM: Homo sapiens
65 (ix) FEATURE:
66 (A) NAME/KEY: CDS
67 (B) LOCATION:1..474
68 (C) IDENTIFICATION METHOD: experimental
69 (D) OTHER INFORMATION:/codon_start= 1
70 /function= "Antigen"
71 /product= "TNF-alpha analog"
72 /evidence= EXPERIMENTAL
73 /gene= "tnfP2-1"
74 /standard_name= "TNF2-1"
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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79 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn
80 1 5 10 15
82 TCT AAA TTC ATC GGT ATA ACT GAG CTG CAG CTC CAG TGG CTG AAC CGC 96
83 Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg
84 20 25 30
86 CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG 144
87 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
88 35 40 45
90 CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC 192
91 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
92 50 55 60
94 TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC 240
95 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
96 65 70 75 80
98 ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT 288
99 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
100 85 90 95
102 GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC 336
103 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
104 100 105 110
106 AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG 384
107 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
108 115 120 125
110 AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC 432
111 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
112 130 135 140
114 TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC 474
115 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
116 145 150 155
119 (2) INFORMATION FOR SEQ ID NO: 2:
121 (i) SEQUENCE CHARACTERISTICS:
122 (A) LENGTH: 158 amino acids
123 (B) TYPE: amino acid
124 (D) TOPOLOGY: linear

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126 (ii) MOLECULE TYPE: protein
128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
130 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Gln Tyr Ile Lys Ala Asn
131 1 5 10 15
133 Ser Lys Phe Ile Gly Ile Thr Glu Leu Gln Leu Gln Trp Leu Asn Arg
134 20 25 30
136 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
137 35 40 45
139 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
140 50 55 60
142 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
143 65 70 75 80
145 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
146 85 90 95
148 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
149 100 105 110
151 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
152 115 120 125
154 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
155 130 135 140
157 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
158 145 150 155
161 (2) INFORMATION FOR SEQ ID NO: 3:
163 (i) SEQUENCE CHARACTERISTICS:
164 (A) LENGTH: 474 base pairs
165 (B) TYPE: nucleic acid
166 (C) STRANDEDNESS: double
167 (D) TOPOLOGY: linear
169 (ii) MOLECULE TYPE: DNA (genomic)
171 (iii) HYPOTHETICAL: NO
173 (iv) ANTI-SENSE: NO
175 (vi) ORIGINAL SOURCE:
176 (A) ORGANISM: Homo sapiens
178 (ix) FEATURE:
179 (A) NAME/KEY: CDS
180 (B) LOCATION: 1..474
181 (D) OTHER INFORMATION: /codon_start= 1
182 /function= "Antigen"
183 /product= "TNF-alpha analog"
184 /gene= "tnfP2-3"
185 /standard_name= "TNF2-3"
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
189 ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT 48
190 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
W--> 191 160 165 170 175
193 GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC 96
194 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
W--> 195 180 185 190
197 CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG 144

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198 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 W--> 199 195 200 205
 201 CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC 192
 202 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 W--> 203 210 215 220
 205 TTC CAG TAC ATA AAG GCC AAC TCC AAG TTT ATC GGC ATC ACC GAG CTC 240
 206 Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
 W--> 207 225 230 235
 209 ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT 288
 210 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 W--> 211 240 245 250 255
 213 GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC 336
 214 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 W--> 215 260 265 270
 217 AAG CCC TGG TAT GAG CCC ATC TAT CTG GGA GGG GTC TTC CAG CTG GAG 384
 218 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 W--> 219 275 280 285
 221 AAG GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC 432
 222 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 W--> 223 290 295 300
 225 TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC
 226 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu 474
 W--> 227 305 310 315
 230 (2) INFORMATION FOR SEQ ID NO: 4:
 232 (i) SEQUENCE CHARACTERISTICS:
 233 (A) LENGTH: 158 amino acids
 234 (B) TYPE: amino acid
 235 (D) TOPOLOGY: linear
 237 (ii) MOLECULE TYPE: protein
 239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 241 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 242 1 5 10 15
 244 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 245 20 25 30
 247 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 248 35 40 45
 250 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 251 50 55 60
 253 Phe Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
 254 65 70 75 80
 256 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 257 85 90 95
 259 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 260 100 105 110
 262 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 263 115 120 125
 265 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 266 130 135 140
 268 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu

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Input Set : A:\US09060294.txt
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269 145 150 155
 272 (2) INFORMATION FOR SEQ ID NO: 5:
 274 (i) SEQUENCE CHARACTERISTICS:
 275 (A) LENGTH: 474 base pairs
 276 (B) TYPE: nucleic acid
 277 (C) STRANDEDNESS: double
 278 (D) TOPOLOGY: linear
 280 (ii) MOLECULE TYPE: DNA (genomic)
 282 (iii) HYPOTHETICAL: NO
 284 (iv) ANTI-SENSE: NO
 286 (vi) ORIGINAL SOURCE:
 287 (A) ORGANISM: Homo sapiens
 289 (ix) FEATURE:
 290 (A) NAME/KEY: CDS
 291 (B) LOCATION: 1..474
 292 (D) OTHER INFORMATION: /codon_start= 1
 293 /function= "Antigen"
 294 /product= "TNF-alpha analog"
 295 /gene= "tnfP2-4"
 296 /standard_name= "TNF2-4"
 298 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 300 ATG GTC AGA TCA TCT TCT CGA ACC CCG AGT GAC AAG CCT GTA GCC CAT 48
 301 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 W--> 302 160 165 170 175
 304 GTT GTA GCA AAC CCT CAA GCT GAG GGG CAG CTC CAG TGG CTG AAC CGC 96
 305 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 W--> 306 180 185 190
 308 CGG GCC AAT GCC CTC CTG GCC AAT GGC GTG GAG CTG AGA GAT AAC CAG 144
 309 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 W--> 310 195 200 205
 312 CTG GTG GTG CCA TCA GAG GGC CTG TAC CTC ATC TAC TCC CAG GTC CTC 192
 313 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 W--> 314 210 215 220
 316 TTC AAG GGC CAA GGC TGC CCC TCC ACC CAT GTG CTC CTC ACC CAC ACC 240
 317 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
 W--> 318 225 230 235
 320 ATC AGC CGC ATC GCC GTC TCC TAC CAG ACC AAG GTC AAC CTC CTC TCT 288
 321 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 W--> 322 240 245 250 255
 324 GCC ATC AAG AGC CCC TGC CAG AGG GAG ACC CCA GAG GGG GCT GAG GCC 336
 325 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 W--> 326 260 265 270
 328 AAG CCC CAG TAT ATC AAG GCC AAT TCG AAA TTC ATC GGC ATC ACG GAG 384
 329 Lys Pro Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
 W--> 330 275 280 285
 332 CTC GGT GAC CGA CTC AGC GCT GAG ATC AAT CGG CCC GAC TAT CTC GAC 432
 333 Leu Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 W--> 334 290 295 300
 335 TTT GCC GAG TCT GGG CAG GTC TAC TTT GGG ATC ATT GCC CTC 474

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/060,294B

DATE: 01/03/2005

TIME: 16:38:45

Input Set : A:\US09060294.txt

Output Set: N:\CRF4\01032005\I060294B.raw

L:23 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
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L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
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L:447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
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L:558 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:633 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:637 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
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L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

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Input Set : A:\US09060294.txt
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L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
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L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11